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B

PCR Fragg./ CDNA clones	nt. positions
PCR1	388-731
PCR2	1575-1774
PCR3	388-1774
5'RACE	1-540
G6 library	1-641
1.1	53-1007
1.2	1018-2188
1.3	1553-2563
2.1	451-3837
2.2	1590-3983
2.3	2315-3983

A

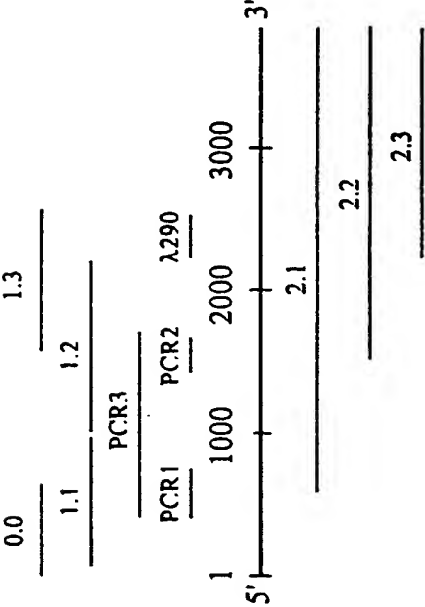


Fig. 1

SUBSTITUTE SHEET (RULE 26)

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F S S H V V E D G V L L G A V G A Y D W N G A V L K E T S A G K V I P L R E S Y 410

CTGAAGAGTTCGCCGAGGAGCTCAAGAACCATGGTGCATACCTTGGGTATCACAGTACAGTTCGGGTGTCTCTCCAGGAGGCGGAGTGATCTGGCCGGAGCCGCCCGTTCACACCAC 1410
L K E F P E E L K N H G A Y L G Y T V T S V V S S R Q G R V Y V A G A P R F N H 450

ACGGCAAGGTATCTGTTCACCATGCACACACACCGGAGCCTCACCATCCACAGGCTATCCCGGGCCAGCAGATAGGCTCTTACTTTGGAGTGAATCACCTTCGGTGGACATCGAC 1560
T G K V I L F T M H N N R S L T I H Q A M R G Q Q I G S Y F G S E I T S V P I D 490

GGCAGCGCGTGACTGATGCTCTGCTGGTGGGGCACCCATGTACTTCACGAGGGCGGTGAGCGAGGCAAGGTGTAGCTCTATGAGTGTGAGACAGAAACCGGTTTGTATTATACGGGAACG 1680
G D G V T D V L L V G A P H Y F N E G R E R G K V Y V Y E L R Q N R F V Y N G T 530

CTAAGGATTCACACAGTACACAGAAATGCCGATTTGGTCTCCATTGCCCTCAGTTCGACAGCCTCAACAGGATTCCTACATGACGTGGTGGAGCCGCCCTGGAGGACAAACCAC 1900
L K D S H S Y Q N A R F G S S I A S V R D L N O D S Y N D V V V G A P L E D N H 570

GCAGAGCCATCTACATCTTCACGGCTTCGAGCGGAGCATCCTGAAGACACCTAAGACAGAAATCACAGCTGGCTACCGGCTCCAGTATTTTGGTGCAGCATCCACGGG 1920
A G A I Y I F H G F R G S I L K T P K Q R I T A S E L A T G L Q Y F G C S I H G 610

CAATTGGACCTCAATGAGGATGGGCTCATCGACCTGGCAGTGGAGCCCTTGGCAACGCTGTGATCTGTGGTCCCGCCAGTGGTTCAGATCAATGCCAGCCCTCCACCTTTGAGGCATCC 2040
Q L D L N E D G L I D L A V G A L G N A V I L W S R P V V Q I N A S L H F E P S 650

AAGATCAATCTTCCACAGAGACTGCAAGCGGAGTGCGAGGGATGCCAGCTGGCTGGCGCCTTCCTCTGCTTCACGCCCATCTTCCTGGCACCCCATTTCCAAACACAACTGTGGC 2160
K I N I F H R D C K R S G R D A T C L A A F L C F T P I F L A P H F Q T T T V G 690

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I I R Y N A T M D E R R Y T P R A H L D E G G D R F T N R A V L L S S G Q E L C E 730

CGGATCAATCTCCATGCTCTGGACACTGCTGACTAGTGAAGCCAGTGAACCTTCTCAGTCGAGTATCCCTGGAGGACCTTGACCATGGCCCCATGCTGGACGACGGCTGGCCACCACCT 2400
R I N F H V L D T A D Y V K P V T F S V E Y S L E D P D H G P H L D D G W P T T 770

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AGGAGGCTCGCGAGGACTGCTCCGCATACAGCTGTCTTCGACACACACAGTCTTCATATGAGAGGCACACGCGCAGGAGTGGCGGTGGAGGCCACACTGGAGAAACAGGGGCGAGAAC 2640
R K P A Q D C S A Y T L S F D T T V F I I E S T R Q R V A V E A T L E N R G E N 850

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Fig 2c

GCCTACAGTACGGTCTTAATATCTCGCAGTCAGCAACCTGCAGTTTGCCAGCTTGATCCAGAAAGGAGGACTCAGACGGTAGCATTGAGTGTGTAACGAGGAGGCTCCAGNAG 2760
A Y S T V L N[•] I S Q S A N L Q F A S L I Q K E D S D G S I E C V N E E R R L Q K 890

CAACTCTGCAACGTCAGCTATCCCTTCTTCCGGGGCAAGGCCAAGGTGGCTTTCGGTCTTGATTCCGAGTTCAGCAATCCATCTTCTACACCACCTGGAGATCGAGCTCGCTGCAGGC 2880
Q V C N[•] V S Y P F F R A K A K V A F R L D S E F S K S I F L H L E I E L A A G 930

AGTGACAGTAAATGAGCGGACAGCACCAAGGAAGACAACTGGCCCTTACGCTCCACCTCAATACGAGGCTGACGTCCTCTTACCAGGAGCAGCAGCTGAGCCACTAGCAGGTC 3000
S D S N E R D S T K E D N V A P L R F H L K Y E A D V L F T R S S L S H Y E V 970

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I A T R S G N R L L K L R D F L T D E A N[•] T S C N I W G N[•] S T E Y R P T P V E E 1050

GACTTGGGTGCTGCTCCACAGCTGAATCAGACGCAACTCTGATGTGCTCTCCATCAACTGCAATATACGGTGGTCCCAACCAAGGGAATCAATTTCCATCTACTGGGAACCTGTGGTTG 3360
D L R R A P Q L N[•] H S N S D V V S I N C N I R L V P N Q E I N F H L L G N L W L 1090

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R S L K A L K Y K S M K I M V N A A L Q R Q F H S P F I F R E E D P S R Q I E F 1130

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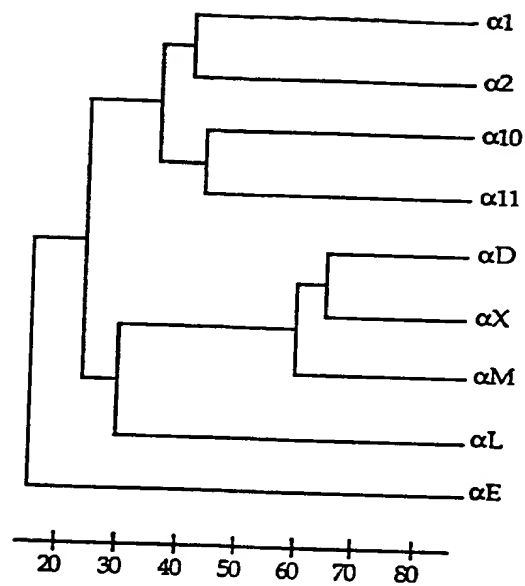
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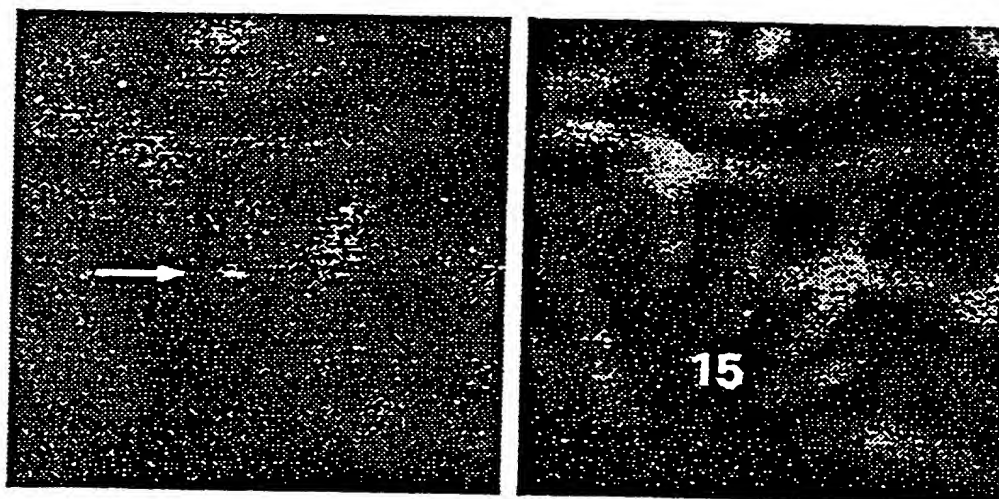
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**Fig. 3**

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A



B

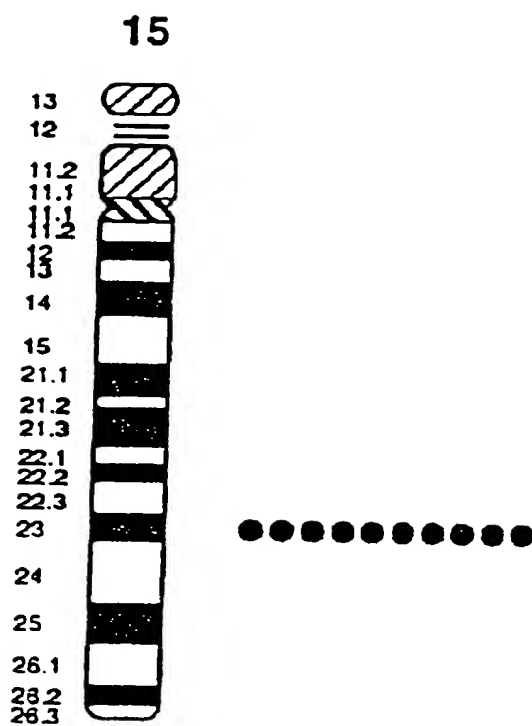


FIG. 4

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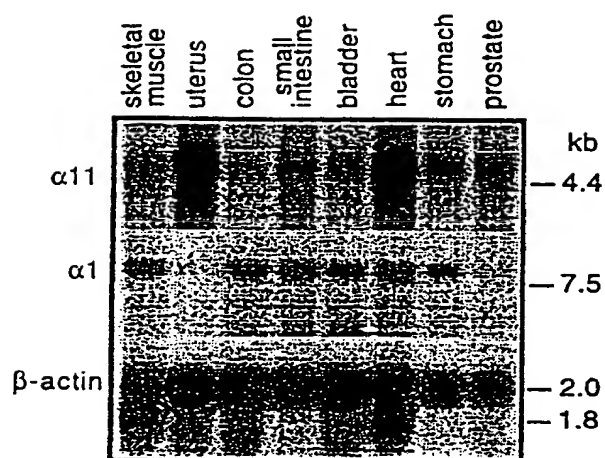


Fig. 5

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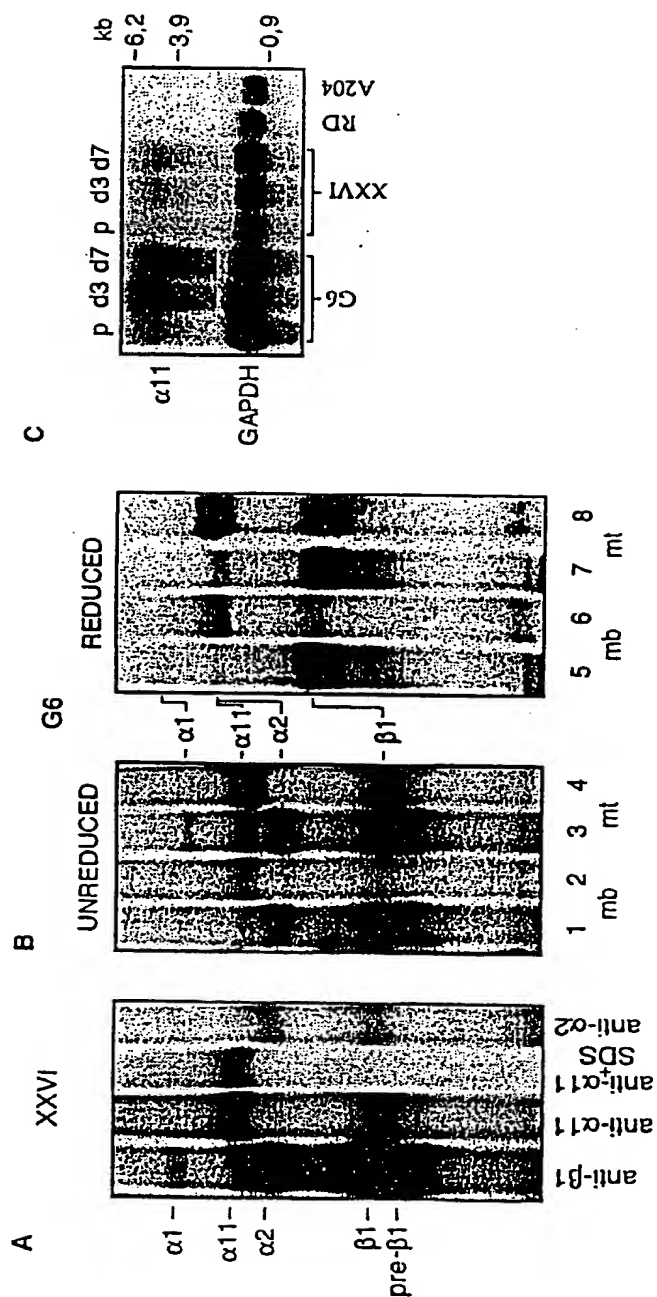


Fig. 6

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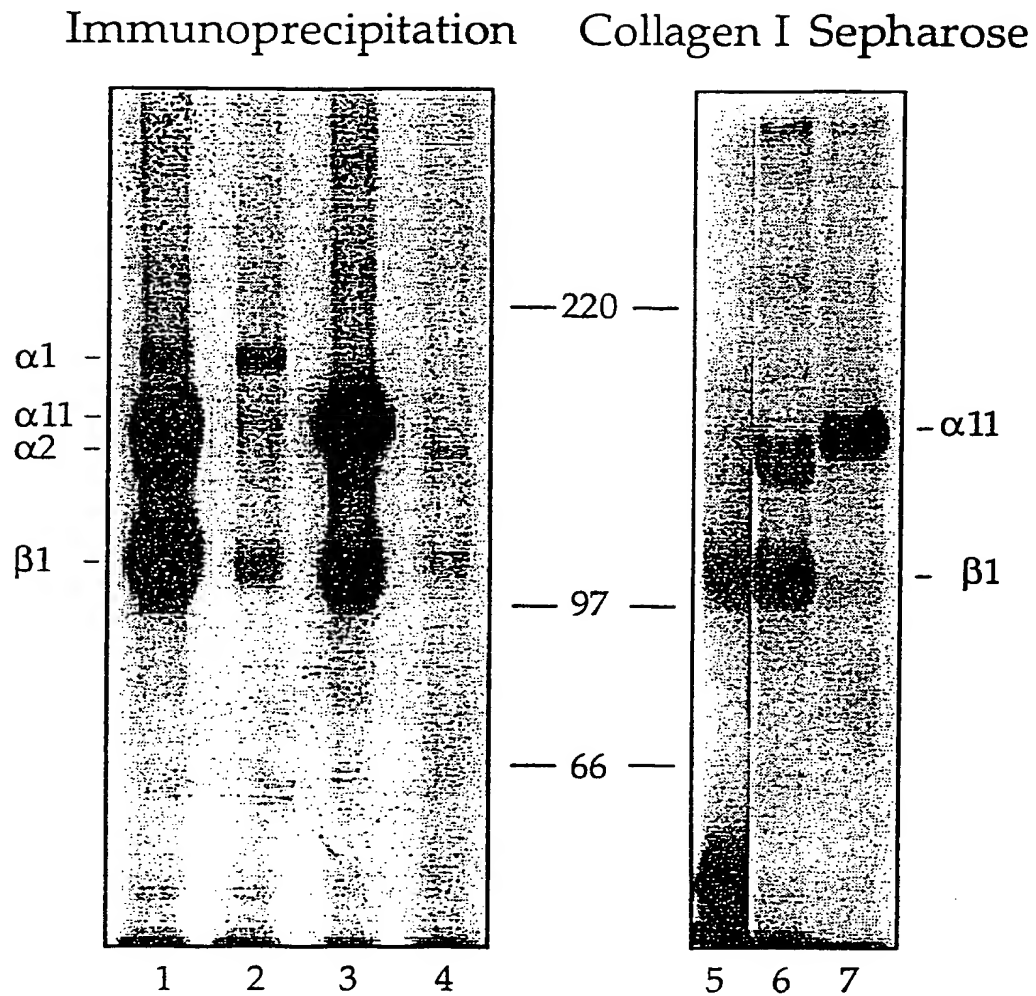


Fig. 7 panel 1

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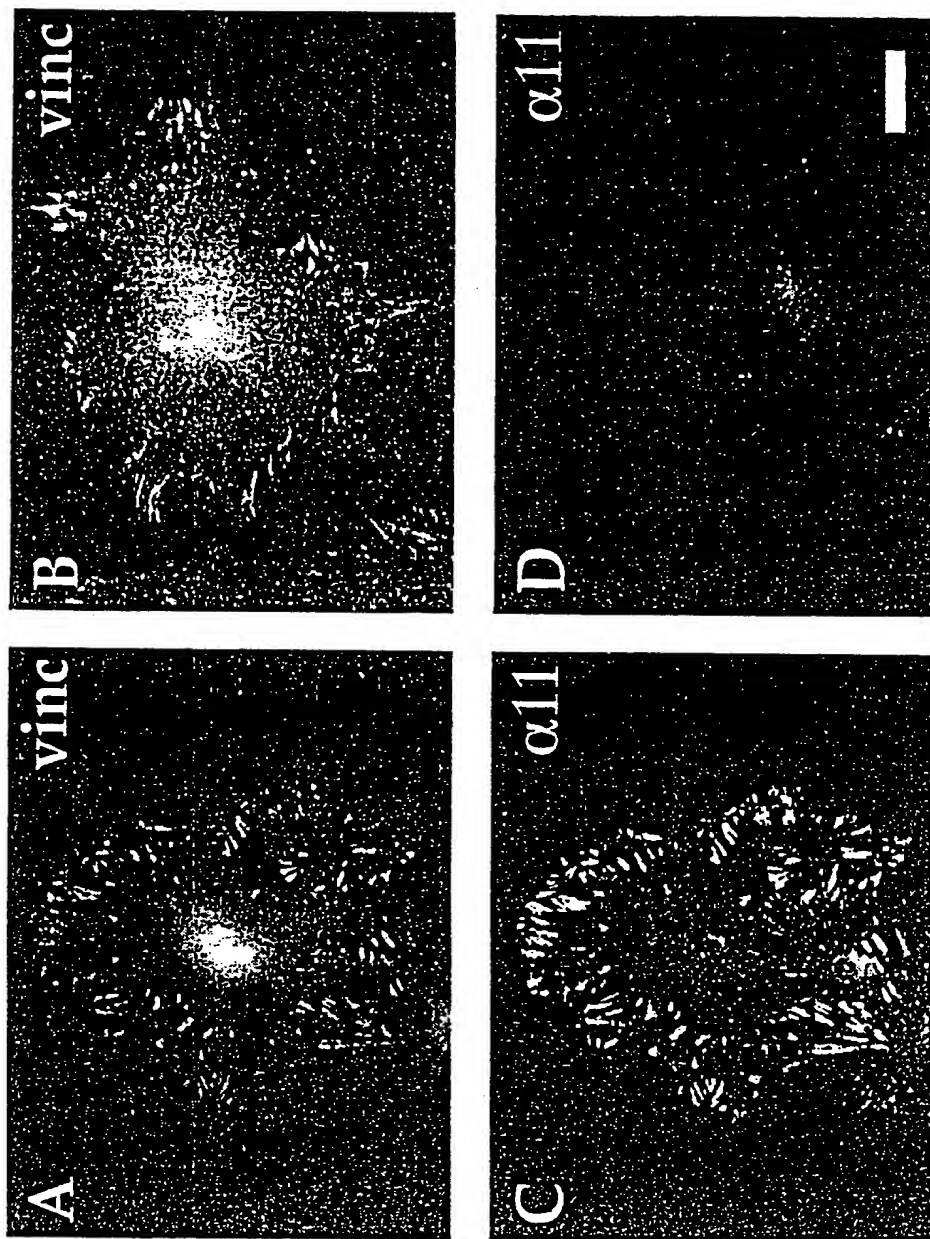


Fig. 7 panel 2

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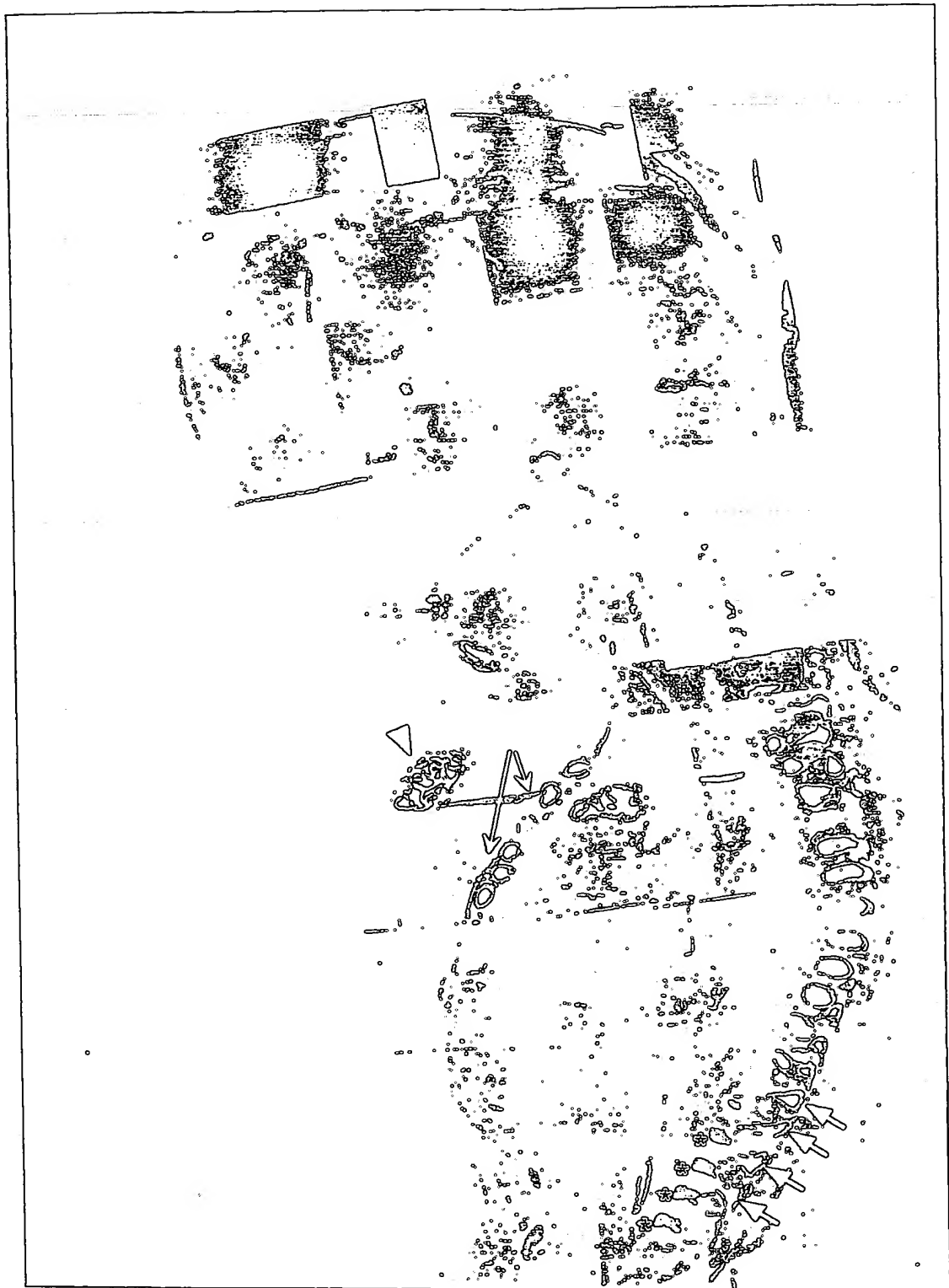


FIG. 8